

SEQUENCE LISTING

<110> CHUGAI SEIYAKU KABUSHIKI KAISHA

5 <120> cDNA and deduced amino acid sequence in human fetus chondrocytes

<130> CGS98-04PCT

10 <160> 22

<170> PatentIn Ver. 2.0

<210> 1

15 <211> 3442

<212> DNA

<213> Homo sapiense

20 <220>

<221> CDS

<222> (49)..(3183)

<400> 1

25 cgccgcagcc gccggcgctg tggagatatt ctctaagccg ctttcac atg gga gaa 57
Met Gly Glu
1

30 ata gag cag agg cag acc cca gga tca cga ctg ggg gcc ccg gaa aat 105
Ile Glu Gln Arg Pro Thr Pro Gly Ser Arg Leu Gly Ala Pro Glu Asn
5 10 15

35 tcg ggg atc agt acc ttg gaa cgt gga cag aag ccg ccc cca aca cct 153
Ser Gly Ile Ser Thr Leu Glu Arg Gly Gln Lys Pro Pro Pro Thr Pro
20 25 30 35

40 tca gga aaa ctc gtg tcc atc aaa atc cag atg ctg gat gac acc cag 201
Ser Gly Lys Leu Val Ser Ile Lys Ile Gln Met Leu Asp Asp Thr Gln
40 45 50

45 gag gca ttt gaa gtt cca caa aga gct cct ggg aag gtg ctg ctg gat 249
Glu Ala Phe Glu Val Pro Gln Arg Ala Pro Gly Lys Val Leu Leu Asp
55 60 65

gca gtt tgc aac cac ctc aac ctc gtg gaa ggt gac tat ttt ggc ctc 297

	Ala Val Cys Asn His Leu Asn Leu Val Glu Gly Asp Tyr Phe Gly Leu	
	70 75 80	
5	gag ttt cct gat cac aaa aag atc acg gtg tgg ctg gat ctc cta aaa Glu Phe Pro Asp His Lys Lys Ile Thr Val Trp Leu Asp Leu Leu Lys	345
	85 90 95	
10	ccc att gtg aaa cag att aga agg cca aag cac gtt gtt gtt aag ttt Pro Ile Val Lys Gln Ile Arg Arg Pro Lys His Val Val Val Lys Phe	393
	100 105 110 115	
15	gtg gtg aaa ttc ttt ccg cct gac cac aca caa ctc caa gaa gaa ctc Val Val Lys Phe Phe Pro Pro Asp His Thr Gln Leu Gln Glu Glu Leu	441
	120 125 130	
20	aca agg tac ctg ttc gcg ctg cag gtg aag cag gac ttg gct caa ggc Thr Arg Tyr Leu Phe Ala Leu Gln Val Lys Gln Asp Leu Ala Gln Gly	489
	135 140 145	
25	agg ttg acg tgt aat gac acc agc gca gct ctc ttg att tca cac att Arg Leu Thr Cys Asn Asp Thr Ser Ala Ala Leu Leu Ile Ser His Ile	537
	150 155 160	
30	gtg caa tct gag att ggg gat ttt gat gaa gcc ttg gac aga gag cac Val Gln Ser Glu Ile Gly Asp Phe Asp Glu Ala Leu Asp Arg Glu His	585
	165 170 175	
35	tta gca aaa aat aaa tac ata cct cag caa gac gca cta gag gac aaa Leu Ala Lys Asn Lys Tyr Ile Pro Gln Gln Asp Ala Leu Glu Asp Lys	633
	180 185 190 195	
40	atc gtg gaa ttt cac cat aac cac att gga caa aca cca gca gaa tca Ile Val Glu Phe His His Asn His Ile Gly Gln Thr Pro Ala Glu Ser	681
	200 205 210	
45	gat ttc cag ctc cta gag att gcc cgt cgg cta gag atg tat gga atc Asp Phe Gln Leu Leu Glu Ile Ala Arg Arg Leu Glu Met Tyr Gly Ile	729
	215 220 225	
50	cgg ttg cac ccg gcc aag gac agg gaa ggc acg aag atc aat ctg gcc Arg Leu His Pro Ala Lys Asp Arg Glu Gly Thr Lys Ile Asn Leu Ala	777
	230 235 240	
55	gtt gcc aac acg gga att cta gtg ttt cag ggt ttc act aag atc aat Val Ala Asn Thr Gly Ile Leu Val Phe Gln Gly Phe Thr Lys Ile Asn	825

	245	250	255			
5	gcc ttc aac tgg gcc aag gtg cgg aag ctg agc ttc aag agg aag cgc Ala Phe Asn Trp Ala Lys Val Arg Lys Leu Ser Phe Lys Arg Lys Arg	260	265	270	275	873
10	ttt ctc atc aag ctc cgg cca gat gcc aat agt gcg tac cag gat acc Phe Leu Ile Lys Leu Arg Pro Asp Ala Asn Ser Ala Tyr Gln Asp Thr	280	285	290		921
15	ttg gaa ttc ctg atg gcc agt cgg gat ttc tgc aag tcc ttc tgg aaa Leu Glu Phe Leu Met Ala Ser Arg Asp Phe Cys Lys Ser Phe Trp Lys	295	300	305		969
20	atc tgt gtt gaa cat cat gcc ttc ttt aga ctt ttt gaa gag ccc aaa Ile Cys Val Glu His His Ala Phe Phe Arg Leu Phe Glu Glu Pro Lys	310	315	320		1017
25	cca aag ccc aag ccc gtc ctc ttt agc cgg ggg tca tca ttt cgg ttc Pro Lys Pro Lys Pro Val Leu Phe Ser Arg Gly Ser Ser Phe Arg Phe	325	330	335		1065
30	agt ggt cgg act cag aag cag gtt ctc gac tat gtt aaa gaa gga gga Ser Gly Arg Thr Gln Lys Gln Val Leu Asp Tyr Val Lys Glu Gly Gly	340	345	350	355	1113
35	cat aag aag gtg cag ttt gaa agg aag cac agc aag att cat tct atc His Lys Lys Val Gln Phe Glu Arg Lys His Ser Lys Ile His Ser Ile	360	365	370		1161
40	cgg agc ctt gct tca cag cct aca gaa ctg aat tcg gaa gtg ctg gag Arg Ser Leu Ala Ser Gln Pro Thr Glu Leu Asn Ser Glu Val Leu Glu	375	380	385		1209
45	cag tct cag cag agc acc agc ctt aca ttt gga gaa ggt gcc gaa tct Gln Ser Gln Gln Ser Thr Ser Leu Thr Phe Gly Glu Gly Ala Glu Ser	390	395	400		1257
50	cca ggg ggc cag agc tgc cgg cga gga aag gaa ccg aag gtt tcc gcc Pro Gly Gly Gln Ser Cys Arg Arg Gly Lys Glu Pro Lys Val Ser Ala	405	410	415		1305
55	ggg gag ccg ggg tcg cac ccg agc cct gcg ccg agg aga agc ccc gcg Gly Glu Pro Gly Ser His Pro Ser Pro Ala Pro Arg Arg Ser Pro Ala	420	425	430	435	1353

	ggt aac aag cag gcg gac gga gcc gcc tcg gcg ccc acg gag gaa gag	1401
	Gly Asn Lys Gln Ala Asp Gly Ala Ala Ser Ala Pro Thr Glu Glu Glu	
	440 445 450	
5		
	gag gag gtc gtt aag gat agg acc cag cag agt aaa cct cag ccc ccg	1449
	Glu Glu Val Val Lys Asp Arg Thr Gln Gln Ser Lys Pro Gln Pro Pro	
	455 460 465	
10		
	cag cca agc aca ggc tcc ctg act ggc agt cct cac ctt tcc gag ctg	1497
	Gln Pro Ser Thr Gly Ser Leu Thr Gly Ser Pro His Leu Ser Glu Leu	
	470 475 480	
15		
	tct gtg aac tcg cag ggg gga gtg gcc cct gcc aac gtg acc ttg tct	1545
	Ser Val Asn Ser Gln Gly Gly Val Ala Pro Ala Asn Val Thr Leu Ser	
	485 490 495	
20		
	ccc aac ctg agc ccc gac acc aag cag gcc tct ccc ttg atc agc ccg	1593
	Pro Asn Leu Ser Pro Asp Thr Lys Gln Ala Ser Pro Leu Ile Ser Pro	
	500 505 510 515	
25		
	ctg ctg aat gac cag gcc tgc ccc cgg acg gac gat gag gat gag ggc	1641
	Leu Leu Asn Asp Gln Ala Cys Pro Arg Thr Asp Asp Glu Asp Glu Gly	
	520 525 530	
30		
	cgg agg aag aga ttc cca act gat aaa gcg tac ttc ata gct aag gaa	1689
	Arg Arg Lys Arg Phe Pro Thr Asp Lys Ala Tyr Phe Ile Ala Lys Glu	
	535 540 545	
35		
	gtg tct acc acc gag cga aca tat ctg aag gat ctc gaa gtt atc act	1737
	Val Ser Thr Thr Glu Arg Thr Tyr Leu Lys Asp Leu Glu Val Ile Thr	
	550 555 560	
40		
	tcg tgg ttt cag agc aca gtg agc aaa gag gac gcc atg ccg gaa gca	1785
	Ser Trp Phe Gln Ser Thr Val Ser Lys Glu Asp Ala Met Pro Glu Ala	
	565 570 575	
45		
	ctg aaa agt ctc ata ttc ccg aat ttt gaa cct ttg cac aaa ttt cat	1833
	Leu Lys Ser Leu Ile Phe Pro Asn Phe Glu Pro Leu His Lys Phe His	
	580 585 590 595	
50		
	act aat ttt ctc aag gaa att gag caa cga ctt gcc ctg tgg gaa ggc	1881
	Thr Asn Phe Leu Lys Glu Ile Glu Gln Arg Leu Ala Leu Trp Glu Gly	
	600 605 610	

	cgc tca aat gcc caa atc aga gat tac caa aga atc ggc gat gtc atg	1929
	Arg Ser Asn Ala Gln Ile Arg Asp Tyr Gln Arg Ile Gly Asp Val Met	
	615 620 625	
5	ctg aag aac att cag ggc atg aag cac ctg gcg gct cac ctg tgg aag	1977
	Leu Lys Asn Ile Gln Gly Met Lys His Leu Ala Ala His Leu Trp Lys	
	630 635 640	
10	cac agc gag gcc ttg gag gcc ctg gag aat gga atc aag agc tcc cgg	2025
	His Ser Glu Ala Leu Glu Ala Leu Glu Asn Gly Ile Lys Ser Ser Arg	
	645 650 655	
15	cgg ctg gag aac ttc tgc aga gac ttt gag ctg cag aag gtg tgt tac	2073
	Arg Leu Glu Asn Phe Cys Arg Asp Phe Glu Leu Gln Lys Val Cys Tyr	
	660 665 670 675	
20	cta ccg ctc aac acc ttc ctc ctg cgg cca ctg cac cgg ctc atg cac	2121
	Leu Pro Leu Asn Thr Phe Leu Leu Arg Pro Leu His Arg Leu Met His	
	680 685 690	
25	tac aag cag gtc ctg gag cgg ctg tgc aaa cac cac ccg ccg agc cac	2169
	Tyr Lys Gln Val Leu Glu Arg Leu Cys Lys His His Pro Pro Ser His	
	695 700 705	
30	gcc gac ttc agg gac tgc cga gcc gct ttg gca gag atc acg gag atg	2217
	Ala Asp Phe Arg Asp Cys Arg Ala Ala Leu Ala Glu Ile Thr Glu Met	
	710 715 720	
35	gtg gca cag ctc cac ggt acg atg atc aag atg gag aat ttc cag aag	2265
	Val Ala Gln Leu His Gly Thr Met Ile Lys Met Glu Asn Phe Gln Lys	
	725 730 735	
40	ctg cac gaa ctc aag aaa gat ttg att ggc att gac aat ctt gtg gtt	2313
	Leu His Glu Leu Lys Lys Asp Leu Ile Gly Ile Asp Asn Leu Val Val	
	740 745 750 755	
45	ccg gga agg gag ttc atc cgt ctg ggc agc ctc agc aag ctc tcg ggg	2361
	Pro Gly Arg Glu Phe Ile Arg Leu Gly Ser Leu Ser Lys Leu Ser Gly	
	760 765 770	
50	aag ggg ctc cag cag cgc atg ttc ttc ctg ttc aac gac gtc ctg cta	2409
	Lys Gly Leu Gln Gln Arg Met Phe Phe Leu Phe Asn Asp Val Leu Leu	
	775 780 785	
55	tac acg agc cgg ggg ctg acg gcc tcc aat cag ttt aaa gtc cac ggg	2457

00955342-0955560

	Tyr	Thr	Ser	Arg	Gly	Leu	Thr	Ala	Ser	Asn	Gln	Phe	Lys	Val	His	Gly	
			790					795					800				
5	cag	ctc	ccg	ctc	tat	ggc	atg	acg	att	gag	gag	agc	gaa	gac	gag	tgg	2505
	Gln	Leu	Pro	Leu	Tyr	Gly	Met	Thr	Ile	Glu	Glu	Ser	Glu	Asp	Glu	Trp	
		805					810					815					
10	ggg	gtg	ccc	cac	tgc	ctg	acc	ctc	cgg	ggc	cag	cgg	cag	tcc	atc	atc	2553
	Gly	Val	Pro	His	Cys	Leu	Thr	Leu	Arg	Gly	Gln	Arg	Gln	Ser	Ile	Ile	
	820					825					830					835	
15	gtg	gcc	gcc	agt	tct	cgg	tcc	gag	atg	gag	aag	tgg	gtt	gag	gac	atc	2601
	Val	Ala	Ala	Ser	Ser	Arg	Ser	Glu	Met	Glu	Lys	Trp	Val	Glu	Asp	Ile	
				840						845					850		
20	cag	atg	gcc	att	gac	ctg	gcg	gag	aag	agc	agc	agc	ccc	gcc	cct	gag	2649
	Gln	Met	Ala	Ile	Asp	Leu	Ala	Glu	Lys	Ser	Ser	Ser	Pro	Ala	Pro	Glu	
				855					860					865			
25	ttc	ctg	gcc	agc	agc	ccc	cct	gac	aac	aag	tcc	cct	gat	gaa	gcc	acc	2697
	Phe	Leu	Ala	Ser	Ser	Pro	Pro	Asp	Asn	Lys	Ser	Pro	Asp	Glu	Ala	Thr	
		870						875					880				
30	gcg	gct	gac	cag	gag	tca	gag	gat	gac	ctg	agc	gcc	tgc	cgc	aca	tgc	2745
	Ala	Ala	Asp	Gln	Glu	Ser	Glu	Asp	Asp	Leu	Ser	Ala	Ser	Arg	Thr	Ser	
		885				890						895					
35	ctg	gag	cgc	cag	gcc	ccg	cac	cgc	ggc	aac	aca	atg	gtg	cac	gtg	tgc	2793
	Leu	Glu	Arg	Gln	Ala	Pro	His	Arg	Gly	Asn	Thr	Met	Val	His	Val	Cys	
	900					905					910					915	
40	tgg	cac	cgc	aac	acc	agc	gtc	tcc	atg	gtg	gac	ttc	agc	atc	gca	gtg	2841
	Trp	His	Arg	Asn	Thr	Ser	Val	Ser	Met	Val	Asp	Phe	Ser	Ile	Ala	Val	
				920						925					930		
45	gag	aat	cag	ttg	tct	gga	aac	ctg	ctg	agg	aaa	ttc	aaa	aac	agc	aac	2889
	Glu	Asn	Gln	Leu	Ser	Gly	Asn	Leu	Leu	Arg	Lys	Phe	Lys	Asn	Ser	Asn	
			935					940					945				
50	ggg	tgg	cag	aag	ctg	tgg	gtg	gtg	ttc	aca	aac	ttc	tgc	ctg	ttc	ttc	2937
	Gly	Trp	Gln	Lys	Leu	Trp	Val	Val	Phe	Thr	Asn	Phe	Cys	Leu	Phe	Phe	
		950						955					960				
55	tac	aaa	tca	cac	cag	gac	aat	cat	ccc	ctt	gcc	agc	ctg	cct	ctg	ctc	2985
	Tyr	Lys	Ser	His	Gln	Asp	Asn	His	Pro	Leu	Ala	Ser	Leu	Pro	Leu	Leu	

009250"24E5550

	965	970	975	
	ggc tac tcg ctc acc atc ccc tct gag tcc gag aac atc cag aaa gac			3033
	Gly Tyr Ser Leu Thr Ile Pro Ser Glu Ser Glu Asn Ile Gln Lys Asp			
5	980	985	990	995
	tac gtg ttc aag ctg cac ttc aag tcc cac gtc tac tac ttc agg gcg			3081
	Tyr Val Phe Lys Leu His Phe Lys Ser His Val Tyr Tyr Phe Arg Ala			
	1000	1005	1010	
10				
	gaa agc gag tac acg ttc gaa agg tgg atg gaa gtg atc cgc agt gcc			3129
	Glu Ser Glu Tyr Thr Phe Glu Arg Trp Met Glu Val Ile Arg Ser Ala			
	1015	1020	1025	
15				
	acc agc tct gcc tcg cga ccc cac gtg ttg agc cac aaa gag tct ctt			3177
	Thr Ser Ser Ala Ser Arg Pro His Val Leu Ser His Lys Glu Ser Leu			
	1030	1035	1040	
	gtg tat tgatggcgg acacactcgt ttccgcagt gctgctttcc tggaagacgt			3233
20	Val Tyr			
	1045			
	ttcctttctt ctgtattaat gaagcctggt aaaattaaca cctgtctgaa aatcaaaaac			3293
25				
	atggttccc agcagctctc ctgtctccac agccgcgttt ttttaacccg acctctcagc			3353
	gtttgaatga acagcgtcc cacctccagt cctggcatcc gctgggggcg ctgttcttta			3413
	gctagtgccg gtattaaaac attgtcatt			3442
30				
	<210> 2			
	<211> 1045			
	<212> PRT			
35	<213> Homo sapiens			
	<400> 2			
	Met Gly Glu Ile Glu Gln Arg Pro Thr Pro Gly Ser Arg Leu Gly Ala			
	1 5 10 15			
40				
	Pro Glu Asn Ser Gly Ile Ser Thr Leu Glu Arg Gly Gln Lys Pro Pro			
	20 25 30			
	Pro Thr Pro Ser Gly Lys Leu Val Ser Ile Lys Ile Gln Met Leu Asp			
45	35 40 45			

009250"2hes550

	Asp Thr Gln Glu Ala Phe Glu Val Pro Gln Arg Ala Pro Gly Lys Val	
	50	55 60
5	Leu Leu Asp Ala Val Cys Asn His Leu Asn Leu Val Glu Gly Asp Tyr	
	65	70 75 80
	Phe Gly Leu Glu Phe Pro Asp His Lys Lys Ile Thr Val Trp Leu Asp	
		85 90 95
10	Leu Leu Lys Pro Ile Val Lys Gln Ile Arg Arg Pro Lys His Val Val	
		100 105 110
	Val Lys Phe Val Val Lys Phe Phe Pro Pro Asp His Thr Gln Leu Gln	
15		115 120 125
	Glu Glu Leu Thr Arg Tyr Leu Phe Ala Leu Gln Val Lys Gln Asp Leu	
		130 135 140
20	Ala Gln Gly Arg Leu Thr Cys Asn Asp Thr Ser Ala Ala Leu Leu Ile	
		145 150 155 160
	Ser His Ile Val Gln Ser Glu Ile Gly Asp Phe Asp Glu Ala Leu Asp	
		165 170 175
25	Arg Glu His Leu Ala Lys Asn Lys Tyr Ile Pro Gln Gln Asp Ala Leu	
		180 185 190
	Glu Asp Lys Ile Val Glu Phe His His Asn His Ile Gly Gln Thr Pro	
30		195 200 205
	Ala Glu Ser Asp Phe Gln Leu Leu Glu Ile Ala Arg Arg Leu Glu Met	
		210 215 220
35	Tyr Gly Ile Arg Leu His Pro Ala Lys Asp Arg Glu Gly Thr Lys Ile	
		225 230 235 240
	Asn Leu Ala Val Ala Asn Thr Gly Ile Leu Val Phe Gln Gly Phe Thr	
		245 250 255
40	Lys Ile Asn Ala Phe Asn Trp Ala Lys Val Arg Lys Leu Ser Phe Lys	
		260 265 270
	Arg Lys Arg Phe Leu Ile Lys Leu Arg Pro Asp Ala Asn Ser Ala Tyr	
45		275 280 285

009250" 2425560

	Gln Asp Thr Leu Glu Phe Leu Met Ala Ser Arg Asp Phe Cys Lys Ser	
	290	295 300
5	Phe Trp Lys Ile Cys Val Glu His His Ala Phe Phe Arg Leu Phe Glu	
	305	310 315 320
	Glu Pro Lys Pro Lys Pro Lys Pro Val Leu Phe Ser Arg Gly Ser Ser	
		325 330 335
10	Phe Arg Phe Ser Gly Arg Thr Gln Lys Gln Val Leu Asp Tyr Val Lys	
		340 345 350
	Glu Gly Gly His Lys Lys Val Gln Phe Glu Arg Lys His Ser Lys Ile	
15		355 360 365
	His Ser Ile Arg Ser Leu Ala Ser Gln Pro Thr Glu Leu Asn Ser Glu	
		370 375 380
20	Val Leu Glu Gln Ser Gln Gln Ser Thr Ser Leu Thr Phe Gly Glu Gly	
		385 390 395 400
	Ala Glu Ser Pro Gly Gly Gln Ser Cys Arg Arg Gly Lys Glu Pro Lys	
		405 410 415
25	Val Ser Ala Gly Glu Pro Gly Ser His Pro Ser Pro Ala Pro Arg Arg	
		420 425 430
	Ser Pro Ala Gly Asn Lys Gln Ala Asp Gly Ala Ala Ser Ala Pro Thr	
30		435 440 445
	Glu Glu Glu Glu Glu Val Val Lys Asp Arg Thr Gln Gln Ser Lys Pro	
		450 455 460
35	Gln Pro Pro Gln Pro Ser Thr Gly Ser Leu Thr Gly Ser Pro His Leu	
		465 470 475 480
	Ser Glu Leu Ser Val Asn Ser Gln Gly Gly Val Ala Pro Ala Asn Val	
		485 490 495
40	Thr Leu Ser Pro Asn Leu Ser Pro Asp Thr Lys Gln Ala Ser Pro Leu	
		500 505 510
	Ile Ser Pro Leu Leu Asn Asp Gln Ala Cys Pro Arg Thr Asp Asp Glu	
45		515 520 525

009250" 2455550

Asp Glu Gly Arg Arg Lys Arg Phe Pro Thr Asp Lys Ala Tyr Phe Ile
530 535 540

5 Ala Lys Glu Val Ser Thr Thr Glu Arg Thr Tyr Leu Lys Asp Leu Glu
545 550 555 560

Val Ile Thr Ser Trp Phe Gln Ser Thr Val Ser Lys Glu Asp Ala Met
565 570 575

10 Pro Glu Ala Leu Lys Ser Leu Ile Phe Pro Asn Phe Glu Pro Leu His
580 585 590

15 Lys Phe His Thr Asn Phe Leu Lys Glu Ile Glu Gln Arg Leu Ala Leu
595 600 605

Trp Glu Gly Arg Ser Asn Ala Gln Ile Arg Asp Tyr Gln Arg Ile Gly
610 615 620

20 Asp Val Met Leu Lys Asn Ile Gln Gly Met Lys His Leu Ala Ala His
625 630 635 640

Leu Trp Lys His Ser Glu Ala Leu Glu Ala Leu Glu Asn Gly Ile Lys
645 650 655

25 Ser Ser Arg Arg Leu Glu Asn Phe Cys Arg Asp Phe Glu Leu Gln Lys
660 665 670

30 Val Cys Tyr Leu Pro Leu Asn Thr Phe Leu Leu Arg Pro Leu His Arg
675 680 685

Leu Met His Tyr Lys Gln Val Leu Glu Arg Leu Cys Lys His His Pro
690 695 700

35 Pro Ser His Ala Asp Phe Arg Asp Cys Arg Ala Ala Leu Ala Glu Ile
705 710 715 720

Thr Glu Met Val Ala Gln Leu His Gly Thr Met Ile Lys Met Glu Asn
725 730 735

40 Phe Gln Lys Leu His Glu Leu Lys Lys Asp Leu Ile Gly Ile Asp Asn
740 745 750

45 Leu Val Val Pro Gly Arg Glu Phe Ile Arg Leu Gly Ser Leu Ser Lys
755 760 765

009250" 2455550

	Leu Ser Gly Lys Gly Leu Gln Gln Arg Met Phe Phe Leu Phe Asn Asp	
	770	775 780
5	Val Leu Leu Tyr Thr Ser Arg Gly Leu Thr Ala Ser Asn Gln Phe Lys	
	785	790 795 800
	Val His Gly Gln Leu Pro Leu Tyr Gly Met Thr Ile Glu Glu Ser Glu	
		805 810 815
10	Asp Glu Trp Gly Val Pro His Cys Leu Thr Leu Arg Gly Gln Arg Gln	
		820 825 830
	Ser Ile Ile Val Ala Ala Ser Ser Arg Ser Glu Met Glu Lys Trp Val	
15		835 840 845
	Glu Asp Ile Gln Met Ala Ile Asp Leu Ala Glu Lys Ser Ser Ser Pro	
		850 855 860
20	Ala Pro Glu Phe Leu Ala Ser Ser Pro Pro Asp Asn Lys Ser Pro Asp	
		865 870 875 880
	Glu Ala Thr Ala Ala Asp Gln Glu Ser Glu Asp Asp Leu Ser Ala Ser	
		885 890 895
25	Arg Thr Ser Leu Glu Arg Gln Ala Pro His Arg Gly Asn Thr Met Val	
		900 905 910
	His Val Cys Trp His Arg Asn Thr Ser Val Ser Met Val Asp Phe Ser	
30		915 920 925
	Ile Ala Val Glu Asn Gln Leu Ser Gly Asn Leu Leu Arg Lys Phe Lys	
		930 935 940
35	Asn Ser Asn Gly Trp Gln Lys Leu Trp Val Val Phe Thr Asn Phe Cys	
		945 950 955 960
	Leu Phe Phe Tyr Lys Ser His Gln Asp Asn His Pro Leu Ala Ser Leu	
		965 970 975
40	Pro Leu Leu Gly Tyr Ser Leu Thr Ile Pro Ser Glu Ser Glu Asn Ile	
		980 985 990
	Gln Lys Asp Tyr Val Phe Lys Leu His Phe Lys Ser His Val Tyr Tyr	
45		995 1000 1005

Phe Arg Ala Glu Ser Glu Tyr Thr Phe Glu Arg Trp Met Glu Val Ile
 1010 1015 1020

5 Arg Ser Ala Thr Ser Ser Ala Ser Arg Pro His Val Leu Ser His Lys
 025 1030 1035 1040

Glu Ser Leu Val Tyr
 1045

10

<210> 3
 <211> 25
 <212> DNA
 <213> Artificial

15

<220>
 <223> probe

20

<400> 3
 cataccggtg agtggggcaa gactg 25

25

<210> 4
 <211> 20
 <212> DNA
 <213> Artificial

30

<220>
 <223> probe
 <400> 4
 tgcccagttc aggtctctta 20

35

<210> 5
 <211> 20
 <212> DNA
 <213> Artificial

40

<220>
 <223> probe
 <400> 5
 tgctacttca tcgaccccat 20

45

<210> 6
 <211> 20

009250" 2425560

<212> DNA
<213> Artificial

5 <220>
<223> probe

<400> 6
aaagacctca ccctccatct 20

10 <210> 7
<211> 20
<212> DNA
<213> Artificial

15 <220>
<223> probe

<400> 7
gtcgattacg tggagagcta 20

20 <210> 8
<211> 20
<212> DNA
<213> Artificial

25 <220>
<223> probe

<400> 8
atgaacttct tcaccagctc 20

30 <210> 9
<211> 20
<212> DNA
<213> Artificial

35 <220>
<223> probe

40 <400> 9
gtcaaggctg agaacgggaa 20

<210> 10

45 <211> 20

009250-2465560

<212> DNA
<213> Artificial

5 <220>
<223> probe

<400> 10
tccaccaccc tgggtgctgta 20

10 <210> 11

<211> 20
<212> DNA
<213> Artificial

15 <220>
<223> probe

20 <400> 11
atcagaccca gctcccaaag 20

<210> 12

25 <211> 20
<212> DNA
<213> Artificial

30 <220>
<223> probe

<400> 12
cacagaccca gctcccaaac 20

35 <210> 13

<211> 20
<212> DNA
<213> Artificial

40 <220>
<223> probe

<400> 13
ccttcaggaa aactcgtgtc 20

45

009250"2HE95560
0955342.052600

<210> 14

<211> 20
<212> DNA
5 <213> Artificial

<220>
<223> probe

10 <400> 14
ttggagttgt gtgtggtcag 20

<210> 15

15 <211> 25
<212> DNA
<213> Artificial

<220>
20 <223> probe

<400> 15
gccaaaatag tcaccttcca cgagg 25

25 <210> 16

<211> 20
<212> DNA
<213> Artificial
30

<220>
<223> probe

<400> 16
35 ccttcaggaa aactcgtgtc 20

<210> 17

<211> 29
40 <212> DNA
<213> Artificial

<220>
<223> probe
45

009250"24E5560

<400> 17
aaacgraaga aygtrtgrtg ytcwacaca 29

<210> 18

5

<211> 20
<212> DNA
<213> Artificial

10

<220>
<223> probe

<400> 18
ttccagctcc tagagattgc 20

15

<210> 19

<211> 20
<212> DNA
<213> Artificial

20

<220>
<223> probe

25

<400> 19
tcgtcttcgc tctcctcaat 20

<210> 20

30

<211> 23
<212> DNA
<213> Artificial

35

<220>
<223> probe

<400> 20
cgggtaacaa gcaggcggac gga 23

40

<210> 21

<211> 20
<212> DNA
<213> Artificial

45

<220>

<223> probe

<400> 21

5 tcacttcgtg gtttcagagc 20

<210> 22

<211> 20

10 <212> DNA

<213> Artificial

<220>

<223> probe

15

<400> 22

tcgtcttcgc tctcctcaat 20

009250"2425560